Cytotaxonomical investigations of the Egyptian Compositae (Asteraceae): I - Cardueae and Cichorieae

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Abstract

In this study, karyotype criteria of 30 taxa of the Compositae (Asteraceae) from Egypt representing the two main tribes (Cardueae and Cichorieae) of subfamily Cichorioideae are described and the taxonomic inferences are discussed. Detailed karyotype features were attributed as characters, coded and analysed by NTSYS-pc-program package using UPGMA clustering method. The produced phenograms were also discussed.

Key words: Egyptian Asteraceae, karyotype studies, numerical analysis.

Introduction

The Asteraceae is one of the largest families of angiosperms (1535 genera & 23000 species; BREMER 1994) and is considered by most taxonomists the highest in the scale of evolution. Asteraceae (or Compositae) form an easily recognized and obviously monophyletic group; both morphological and molecular synapomorphies are numerous (BREMER 1987, 1994, 1996, JANSEN et al. 1991, 1992, KARIS 1993, KARIS et al. 1992, KEELEY & JANSEN 1991, KIM et al. 1992).

Many members of the Asteraceae are cosmopolitan, found especially in temperate or tropical montane regions and open and/or dry habitats. Some of the major genera are *Centaurea* (600 species) and *Cirsium* (270) (JUDD et al. 1999). The family is divided into several tribes, which are often arranged into three subfamilies (Barnadesioideae, Cichorioideae and Asteroideae; BREMER 1994).

In the flora of Egypt, the Asteraceae are well represented with 92 genera and 226 species, with most genera within the Cardueae (17) and the Cichorieae (20). The most speciose genera are *Centaurea* (about 15 species) and *Launaea* (about 11 species) (EL-HADIDI & FAYED 1995).

The subfamily Cichorioideae is a paraphyletic group and characterized by style branches with the inner surface stigmatic. Their flowerheads are usually discoid, except in the distinct tribe Lactuceae, which has ligulate heads. Both resin canals and laticifers occur within the subfamily and the latex system is especially well developed in Lactuceae. The Lactuceae are phenetically distinct and have sometimes been placed in their own subfamily (Cronquist 1981, Bremer 1996).

Generic delimitation within the Cardueae (= Cynareae) is problematic. It is quite possible that the larger genera are paraphyletic with some small derivative genera excluded. The distinction between the two large genera *Carduus* and *Cirsium* is dubious, resting on the technical difference between scabrid-barbellate and plumose pappus bristles, respectively. Generic and subtribal classifications within the Cardueae and especially within the Carduinae need a detailed study from a cladistic perspective. The Cardueae are a fairly sizable group with 83 genera and 2500 species (Judd et al. 1999). There are several large genera, each with hundreds of species (e.g. *Centaurea*). The Cardueae comprise four subtribes, viz. two large and about equal-sized subtribes, the Carduinae and the Centaureinae, and the two smaller Carlininae and Echinopsidinae (Bremer 1994).

The Lactuceae (= Cichorieae) are perhaps the best known and most easily recognized tribe of the family. Lettuce (*Lactuca sativa* L.) and endive (*Cichorium endivia* L.) are familiar members of the tribe. The ligulate capitula and the milky latex immediately set the Lactuceae apart from almost all other Asteraceae. The Lactuceae are also known as tribe Cichorieae. They have often been considered a subfamily or even a separate family, but they are now universally considered a tribe well nested within the Asteraceae, with distinctive autapomorphic florets. The Cichorieae comprise 98 genera and more than 1550 species (Judd et al. 1999). Among the largest genera is *Crepis* (200 species). The classification of the Cichorieae into genera and subtribes is in a much better state than in most other tribes of the family. Stebbins (1953) presented a subtribal classification of the Cichorieae, later informally modified by Jeffrey (1966). He classified the tribe into eight subtribes as follows: Scolyminae, Cichoriinae, Microseridinae, Stephanomeriinae, Dendroseridinae, Scorzonerinae, Leontondontinae and Crepidinae (cf. Bremer 1994).

Chromosome numbers are fairly well surveyed in the Lactuceae (Stebbins et al. 1953, Tomb et al. 1978). There is a series of base numbers ranging from x = 10 in *Scolymus* to x = 4 in *Hedypnois*. The base numbers were coded as six unordered character states. The most common number is x = 9. A gradual reduction in base number thus was not assumed initially but comes out as a parsimonious solution in many of the cladograms. The base numbers x = 6 and x = 7 were lumped into one character state, since it is unclear whether some genera (*Leontodon*) have x = 6 or x = 7 (Stebbins 1953).

Chromosomes have been considered as sources of valid taxonomic criteria (MOORE 1978, JACKSON 1984). The karyotype data also appear to be of taxonomic value in providing a logical basis for the redistribution of genera in tribes. Karyotype studies were principally based on the idea that symmetrical karyotypes are more primitive than asymmetrical ones; longer chromosomes more primitive than shorter ones; median centromeres with chromosome arms of equal length were more primitive than chromosomes with arms of unequal length; low basic numbers had given rise to higher ones. These features are based on the comparison between karyotypes of known relative antiquity, as determined through classical taxonomy (SHARMA 1990).

In the present work, chromosome numbers and detailed karyotype features of 30 taxa of Egyptian Asteraceae representing two tribes, Cardueae (8 genera) and Cichorieae (11 genera) were studied. The produced features of the karyotypes were coded and analysed by the NTSYS-pc program package, using UPGMA cluster method (ROHLF 2000). The phenograms produced are discussed in the light of the current systems of classification (BREMER 1994, 1996).

Materials and Methods

Materials of the 30 taxa were collected from various habitats in Egypt. Voucher specimens are deposited at the herbarium of Biological Sciences and Geology Department, Faculty of Education, Ain Shams University, Roxy, Cairo, Egypt.

1. Cytological Studies

Cytological preparations were carried out on root tips obtained from seeds germinated on sterile moist filter paper in Petri dishes at 25° C. Roots were pretreated with 0.05 % colchicine solution for 2–3 hrs. and fixed in Carnoy for 24 hrs. and stored in 70 % ethanol at 4° C. Cytological preparations were made using the Feulgen squash method. The well-spread c-metaphase chromosomes were photographed from temporary preparations at magnifications of 2000x. Slides of the original karyotypes are also preserved in the Laboratory of Cytogenetics of the same department.

A karyogram for each taxon was constructed by arranging the chromosomes in homologous pairs by order of their length and arm ratio as measured from the photographic prints. The number of chromosome types was determined as described by LEVAN et al. (1964). Measurements of chromosome length were taken on the same photographs of the karyogram.

The variation in chromosome length (MCL) and chromosome arm ratio (MAR) within the karyotype have been estimated by calculating the standard error (SE) of these parameters. Karyotype asymmetry deduced from the ratio between the short arms of the chromosomes and their total length was expressed as total form percent (TF %) as

proposed by HUZIWARA (1962). Karyotype asymmetry expressed by the ratio between chromosome arms has been also estimated as the intrachromosomal asymmetry index (A_1) as suggested by ROMERO ZARCO (1986).

The value of A_1 is considered to be close to zero if all chromosomes are metacentric and near to one if all chromosomes are telocentric. Karyotype asymmetry due to the ratio between size of different chromosomes has been also estimated as the interchromosomal asymmetry index (A_2) using PEARSON's dispersion coefficient, that is the ratio between the standard deviation and the mean chromosome length (ROMERO ZARCO 1986).

The existence of previous chromosome counts for the studied taxa has been verified in the indexes of plant chromosome numbers by FEDOROV (1969), GOLDBLATT (1981, 1984, 1985, 1988) and GOLDBLATT & JOHNSON (1990, 1991, 1994, 1996, 1998).

2. Numerical Analysis

For the data analysis, the total number of the recorded attributes (29) in all taxa were scored, combined together in two sets of data and coded for creating the data matrix of computation: (a) Tribe Cardueae and (b) Tribe Cichorieae. The presence or absence of each of the 29 different attributes was treated as a binary character in a data matrix, i.e. coded 1 and 0 respectively (Table 2). The relationships between the studied species, expressed by average taxonomic distance (dissimilarity), have been demonstrated as phenograms, based on the analysis of the recorded characters using the NTSYS program package for IBM-pc as described by ROHLF (2000).

Results

1. Cytological Observations

A. Tribe Cardueae

This tribe is represented in the study by eight genera and 11 species (Table 1, Figs. 1 & 2). Chromosome counts and karyotype description of *Carduus pycnocephalus* were previously reported by KAMEL (1999), whereas the karyotype analyses for both *Centaurea glomerata* and *Notobasis syriaca* were previously reported by KAMEL (2001). Basic chromosome numbers vary between x = 8 in *Amberboa* and *Centaurea aegyptiaca* to x = 17 in the three genera *Notobasis*, *Onopordum* and *Silybum*. In *Carduus pycnocephalus*, x = 9 is recorded, whereas in *Cnicus* and *Echinops* x = 11 and x = 14 are observed (respectively). Three species of the genus *Centaurea* (*C. alexandrina*, *C. calcitrapa* and *C. glomerata*) were found to have x = 10.

The highest MCL among the eleven species of Cardueae was found in *Centaurea calcitrapa* (2.38 ± 0.21 µm), whereas the shortest was observed in *Silybum marianum*

(1.14 ± 0.04 µm). The highest MAR value (1.56 ± 0.09) was recorded in *Centaurea calcitrapa*, whereas the lowest (1.12 ± 0.03) was found in *Onopordum alexandrinum*. The low MAR recorded for the species of the tribe is correlated with high values of the TF % (Table 1), indicating a high degree of karyotype symmetry. However, the A_1 and A_2 values indicate some degree of karyotype asymmetry in two species (*Centaurea aegyptiaca* and *C. calcitrapa*). The A_1 value ranges between 0.10 in *Onopordum alexandrinum* to 0.33 in *Centaurea calcitrapa*, whereas the highest A_2 (0.31) value was found in *Carduus pycnocephalus* and the lowest (0.12) was observed in both *Centaurea alexandrina* and *Notobasis syriaca* (Table 1). *Centaurea calcitrapa* was found to have SAT in its chromosome.

B. Tribe Cichorieae

The chromosome numbers and karyotype description are shown for 19 species of the tribe Cichorieae (Table 1 and Figs. 2–5). The karyotype analyses of the three genera *Garhadiolus*, *Picris* and *Thrincia* were previously reported by KAMEL (1999).

Somatic chromosome number varied between a diploid of $2n = 8$, recorded in the genus *Thrincia,* to a tetraploid of $2n = 32$, recorded in two species of the genus *Launaea* (*L. capitata* and *L. cassiniana*) and in the two species of the genus *Sonchus* (*S. macrocarpus* and *S. oleraceus*). The basic chromosome numbers recorded within the studied species were x = 4, 5, 6, 8, and 9. The basic number of x = 4 was observed in the genus *Thrincia* only, whereas x = 5 was recorded in the two genera *Picris* and *Urospermum*. On the other hand, x = 6 was recorded in the genus *Garhadiolus*. The basic number x = 8 was recorded in 11 species, whereas x = 9 was recorded in four species.

The highest MCL among the studied species of Cichorieae was found in *Garhadiolus* (2.99 ± 0.23 µm), whereas the shortest was observed in *Sonchus oleraceus* (1.30 ± 0.08 µm). The highest MAR value (2.07) was recorded in *Garhadiolus*, whereas the lowest (1.11) was found in the two species of the genus *Sonchus*. Of the studied species, 14 species were found to have TF % above 40 % indicating a high degree of karyotype symmetry. The five species *Cichorium endivia*, *Garhadiolus hedypnois*, *Lactuca sativa*, *Picris damascena* and *Thrincia tripolitana* were found to have asymmetric karyotypes as indicated by the values of A_1 and A_2. Both *Crepis* and *Launaea nudicaulis* were found to have SAT within its chromosomes.

2. Numerical Observations

A. The phenogram of tribe Cardueae

The phenogram obtained (Fig. 6) shows that the examined taxa have a total genetic (taxonomic) distance of about 1.69. At this level, two species of the genus *Centaurea* (*C. aegyptiaca* –3 and *C. calcitrapa* –5) were split off from the other taxa and then distinguished from each other at the level of about 1.33. At the levels 1.47 and 1.35, the

two species *Carduus pycnocephalus* (2) and *Echinops spinosissimus* (8) were split off from the remaining taxa, respectively.

The remaining seven taxa were further split off into two groups at the level of about 1.20. The first group includes three taxa (*Centaurea alexandrina* –4, *Cnicus benedictus* –7 and *Notobasis syriaca* –9), while the second one comprised four taxa (*Amberboa lippii* –1, *Centaurea glomerata* –6, *Onopordum alexandrinum* –10 and *Silybum marianum* –11).

Within the first group, *Notobasis syriaca* (9) was split off from the other taxa at the level of about 1.03. On the other hand, the remaining two taxa (*Centaurea alexandrina* –4 and *Cnicus benedictus* –7) were distinguished from each other at the level of about 0.84. The second group was subdivided at the level of 1.14 into two subgroups. Each of them includes two taxa. The two taxa of the first subgroup (*Onopordum alexandrinum* –10 and *Silybum marianum* –11) were distinguished from each other at the level of about 0.83, whereas, those of the second subgroup (*Amberboa lippii* –1 and *Centaurea glomerata* –6) were distinguished from each other at the level of about 0.71.

B. The phenogram of tribe Cichorieae

Figure 7 demonstrates the phenogram obtained by the analyses of the studied taxa across the data produced through the karyological attributes. As shown in this phenogram, the studied taxa have a total genetic distance of about 1.75. At this level, the studied taxa were split off into two categories. The first category includes only three taxa (*Garhadiolus hedypnois* –14, *Picris damascena* –24 and *Thrincia tripolitana* –29), while the second one comprises the remaining taxa (16 taxa).

Within the first category, *Thrincia tripolitana* (29) was separated from the other two taxa at the level of about 1.40, while *Garhadiolus hedypnois* (14) and *Picris damascena* (24) were distinguished from each other at the level of about 1.13.

Within the second category, *Cichorium endivia* (12), the two species of the genus *Lactuca* (*L. sativa* –16 and *L. serriola* –17) and *Launaea nudicaulis* (21) were grouped together in a small group at the level of about 1.55. Within this group, *Lactuca serriola* (17) and *Launaea nudicaulis* (21) were split off at the level of 1.43 and then distinguished from each other at the level of 0.77. At the level 1.43, the two taxa *Cichorium endivia* (12) and *Lactuca sativa* (16) were further split off.

Of the remaining taxa, *Crepis radicata* (13) was split off at the level of 1.37. Also, *Urospermum picroides* (30) was split off from the rest taxa at the level of 1.25. At the level of 1.00, the two taxa *Hyoseris lucida* (15) and *Sonchus macrocarpus* (27) were split off and then distinguished from each other at 0.82 level. On the other hand, at the level of 0.82, another two taxa were split off (*Launaea tenuiloba* –23 and *Reichardia picroides* –25) and then distinguished from each other at 0.40 level. At the level of 0.75

Sonchus oleraceus (28) was split off from the remaining taxa.

At the level of 0.50, the remaining taxa were divided into two groups, the first one including two species of the genus *Launaea* (*L. capitata* –18 and *L. cassiniana* –19), while the second one comprised three; viz. another two species of *Launaea* (*L. mucronata* –20 and *L. resedifolia* –22) and *Reichardia tingitana* (26).

Discussion

The phenogram produced from the numerical analysis of the studied taxa of tribe Cardueae (Fig. 6) based on 29 karyological characters recorded some relationships within these members.

Centaurea aegyptiaca (3) and *C. calcitrapa* (5) at 1.33 level due to their possessing the highest MCL (2.07 and 2.38 µm).

The separation of *Carduus pycnocephalus* (2) at 1.47 level and *Echinops spinosissimus* (8) at 1.35 level due to their possessing the basic chromosome number of x = 9 and x = 14, respectively.

The clustering of the three taxa, *Notobasis syriaca* (9), *Cnicus benedictus* (7) and *Centaurea alexandrina* (4), at the level of 1.03 due to their possessing the same TF % (42.94, 42.47 and 42.67 %, respectively).

The clustering of the four taxa, *Onopordum alexandrinum* (10), *Silybum marianum* (11), *Amberboa lippii* (1) and *Centaurea glomerata* (6) at the level of 1.14 due to their possessing the highest TF % (47.14, 46.32, 45.52 and 45.77 %, respectively).

On the other hand, the separation of *Onopordum alexandrinum* (10) and *Silybum marianum* (11) at the level of 0.83 due to their possessing the basic chromosome number of x = 17 and their karyotype formula comprising M and m types of chromosomes.

Both *Amberboa lippii* (1) and *Centaurea glomerata* (6) were grouped at the level of 0.71 due to their possessing the same TF % (about 45 %), tetraploid somatic chromosome number ($2n$ = 32 and $2n$ = 48, respectively) and the presence of metacentric (m) type of chromosomes.

As to the members of tribe Cichorieae, the following relationships were recorded from the numerical analysis of the karyological characters (Fig. 7). The clustering of the three taxa, *Thrincia tripolitana* (29), *Garhadiolus hedypnois* (14) and *Picris damascena* (24) at the level of 1.40 due to their possessing low basic chromosome number of x = 4, 6 and 5 (respectively) and longer chromosomes as observed from the values of MCL (1.90, 2.99 and 2.67 µm, respectively).

The clustering of the four taxa *Cichorium endivia* (12), *Lactuca sativa* (16), *Lactuca serriola* (17) and *Launaea nudicaulis* (21) at the level of 1.43 due to their possessing the basic chromosome number of x = 9 within the karyotypes. *Cichorium endivia* (12) and *Lactuca sativa* (16) due to the presence of the low values of TF % (39.88 and 37.69 %), whereas *Lactuca serriola* (17) and *Launaea nudicaulis* (21) at 0.77 level due to the presence of the high values of TF % (42.62 and 42.65 %).

The separation of *Crepis radicata* (13) at 1.37 level due to the possessing of longer chromosomes which characterized its karyotype (MCL = 2.89 ± 0.16 µm), and the presence of the SAT, the separation of *Urospermum picroides* (30) at the level of 1.25 due to the presence of x = 5 with shorter chromosomes (MCL = 1.56 ± 0.06 µm).

Hyoseris lucida (15) and *Sonchus macrocarpus* (27) at 0.82 level due to their possessing similar karyotype symmetry as indicated by TF % values (47.27 and 47.42 %), A_1 (0.10 and 0.09) and A_2 (0.13 and 0.15) (Table 1).

Launaea tenuiloba (23) and *Reichardia picroides* (25) at the level of 0.40 due to their possessing similar MCL (1.72 and 1.74 µm), MAR (1.31) and TF % (43.36 and 43.58 %).

The separation of *Sonchus oleraceus* (28) from the remaining taxa at the level of 0.75 due to the possessing of the shortest chromosomes (MCL = 1.30 ± 0.08 µm) which characterized its karyotype.

The clustering of the five taxa *Launaea capitata* (18), *L. cassiniana* (19), *L. mucronata* (20), *L. resedifolia* (22) and *Reichardia tingitana* (26) at the level of 0.50 due to their possessing the same basic chromosome number (x = 8), high karyotype symmetry (TF % = 46.15, 44.24, 45.14, 44.81 and 45.77 %, respectively) and karyotype formula of metacentric chromosomes (m).

Most of the studied species were found to have metacentric or submetacentric chromosomes indicating that most karyotypes of the Cardueae and Cichorieae are symmetric. It is also indicated that the members of both tribes are primitive.

Most of the karyotypes studied were found to be symmetric (23 species were found to have TF % above 40 %). The value of the TF % for the studied species thus supported previous observations that karyotype in the Asteraceae is symmetric. Longer chromosomes are associated with karyotype asymmetry as revealed by MAR, TF% and A_1 values in both tribes Cardueae and Cichorieae.

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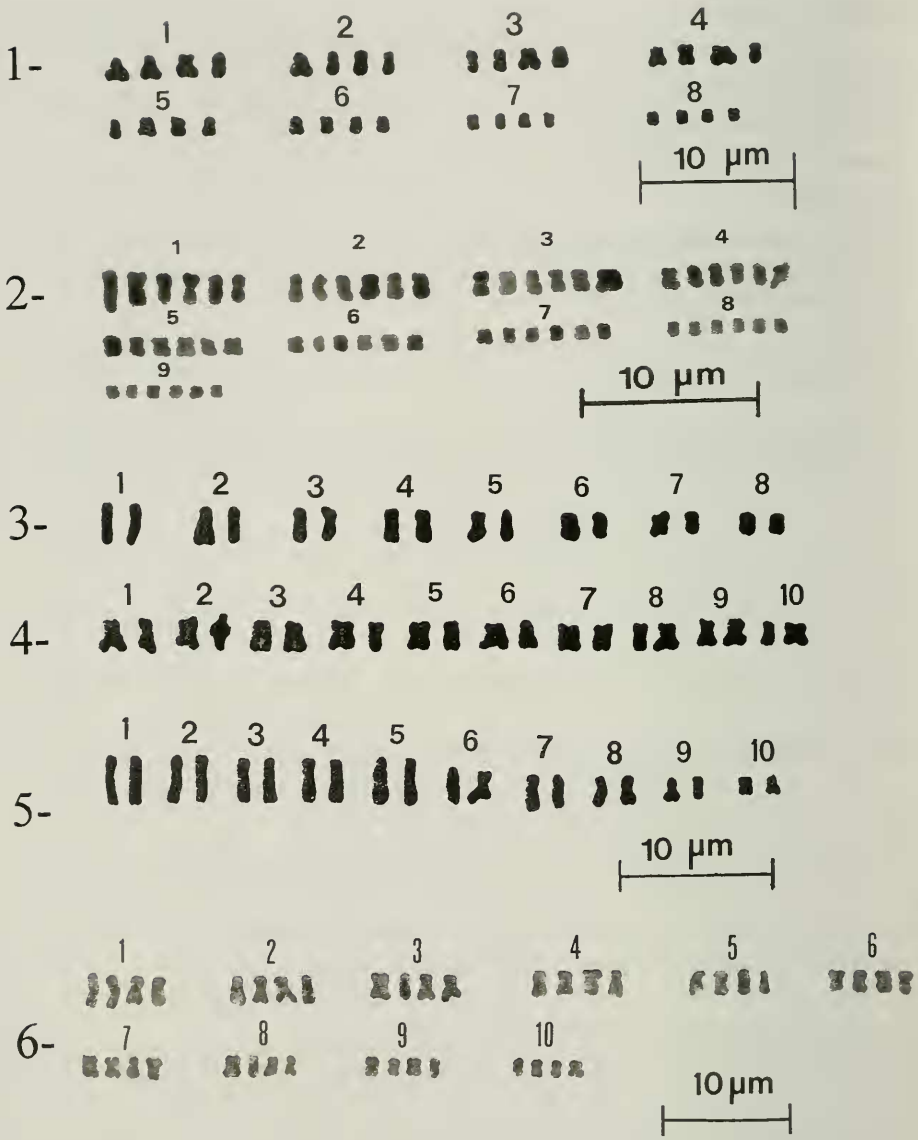

Fig. 1. Karyotype of the studied taxa of tribe Cardueae (Asteraceae)

(1) *Amberboa lippii* (2) *Carduus pycnocephalus*
(3) *Centaurea aegyptiaca* (4) *C. alexandrina*
(5) *C. calcitrapa* (6) *C. glomerata*

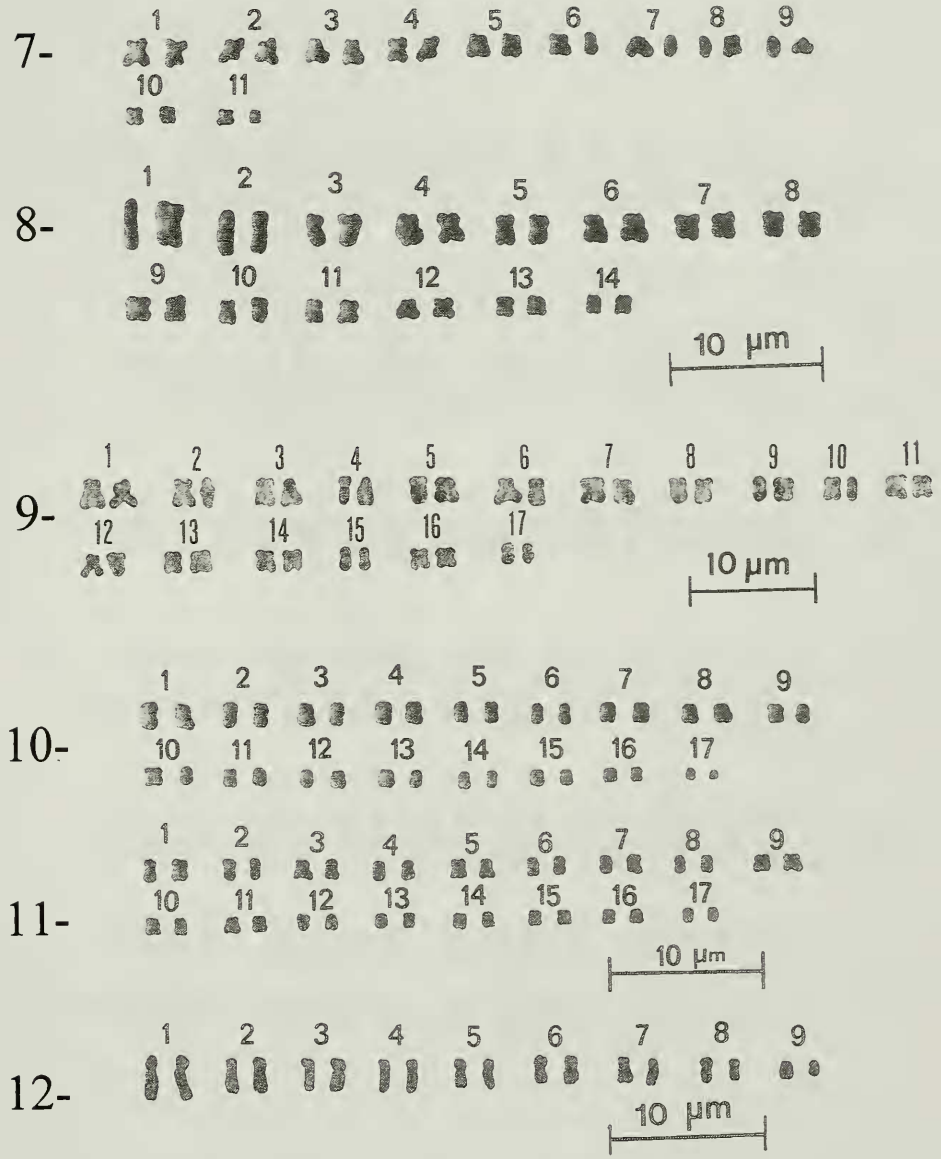

Fig. 2. Karyotype of the studied taxa of tribe Cardueae and Cichorieae (Asteraceae)

(7) *Cnicus benedictus*
(8) *Echinops spinosissimus*
(9) *Notobasis syriaca*
(10) *Onopordum alexandrinum*
(11) *Silybum marianum*
(12) *Cichorium endivia*

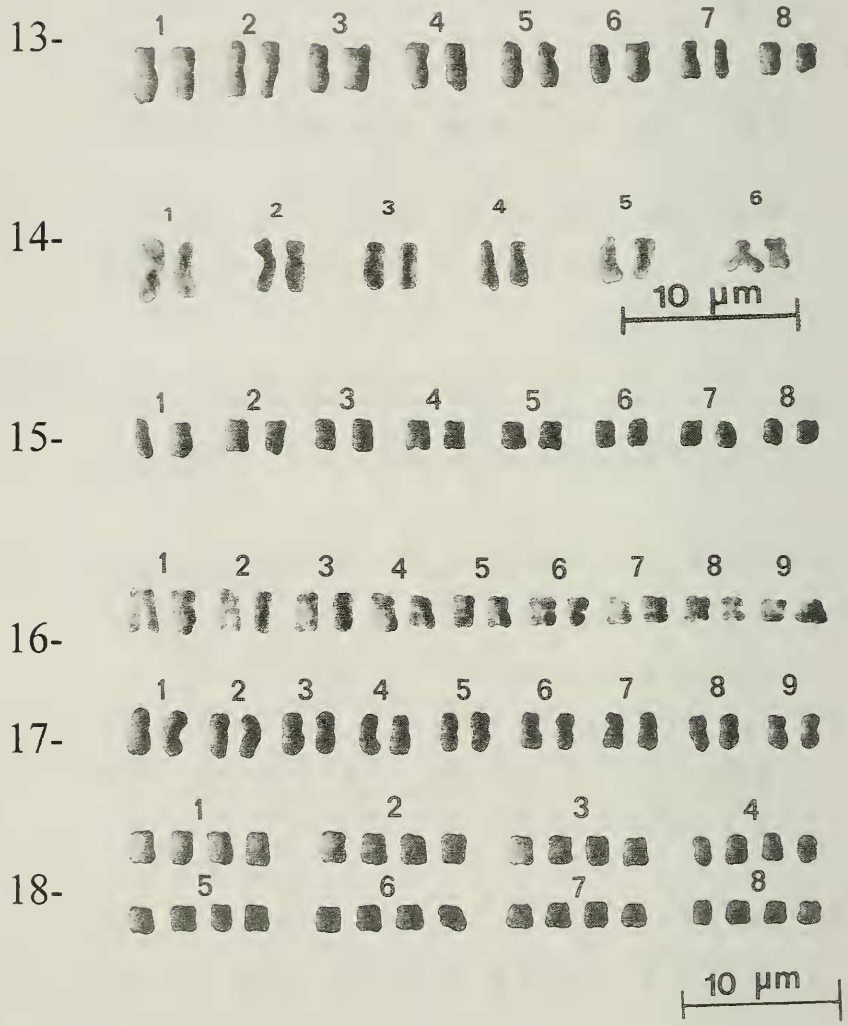

Fig 3. Karyotype of the studied taxa of tribe Cichorieae (Asteraceae)

(13) *Crepis radicata*
(14) *Garhadiolus hedypnois*
(15) *Hyoseris lucida*
(16) *Lactuca sativa*
(17) *L. serriola*
(18) *Launaea capitata*

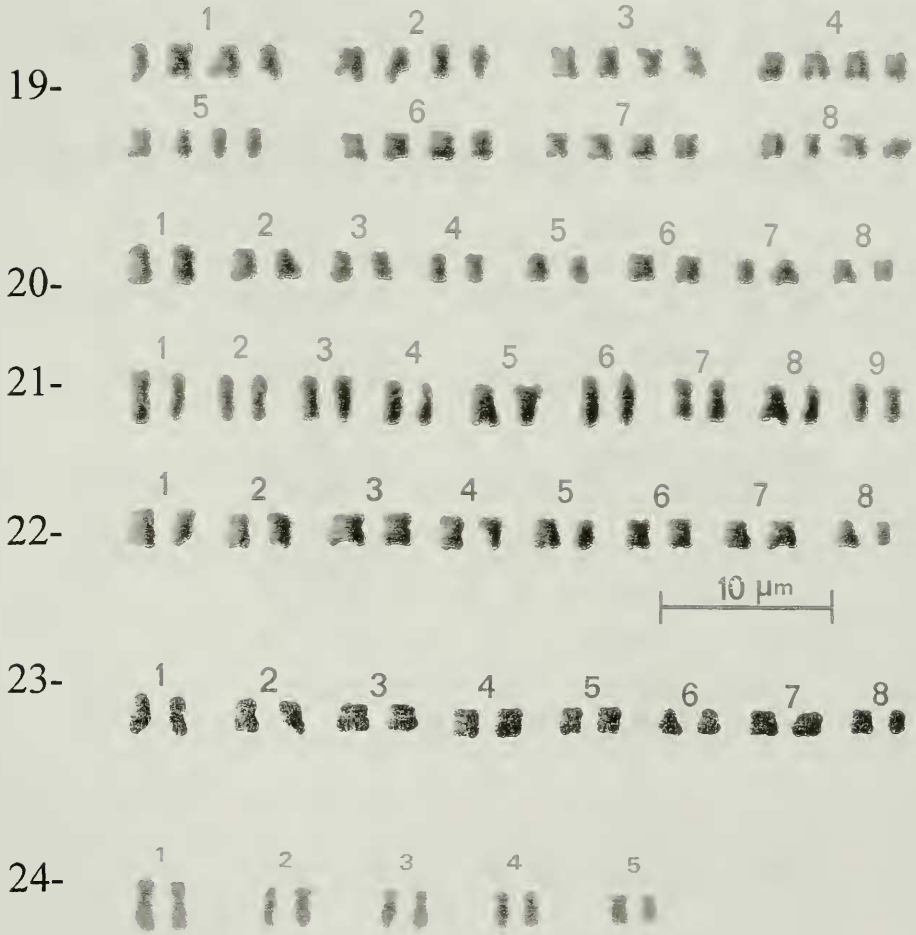

Fig 4. Karyotype of the studied taxa of tribe Cichorieae (Asteraceae)

(19) *Launaea cassiniana*
(20) *L. mucronata*
(21) *L. nudicaulis*
(22) *L. resedifolia*
(23) *L. tenuiloba*
(24) *Picris damascena*

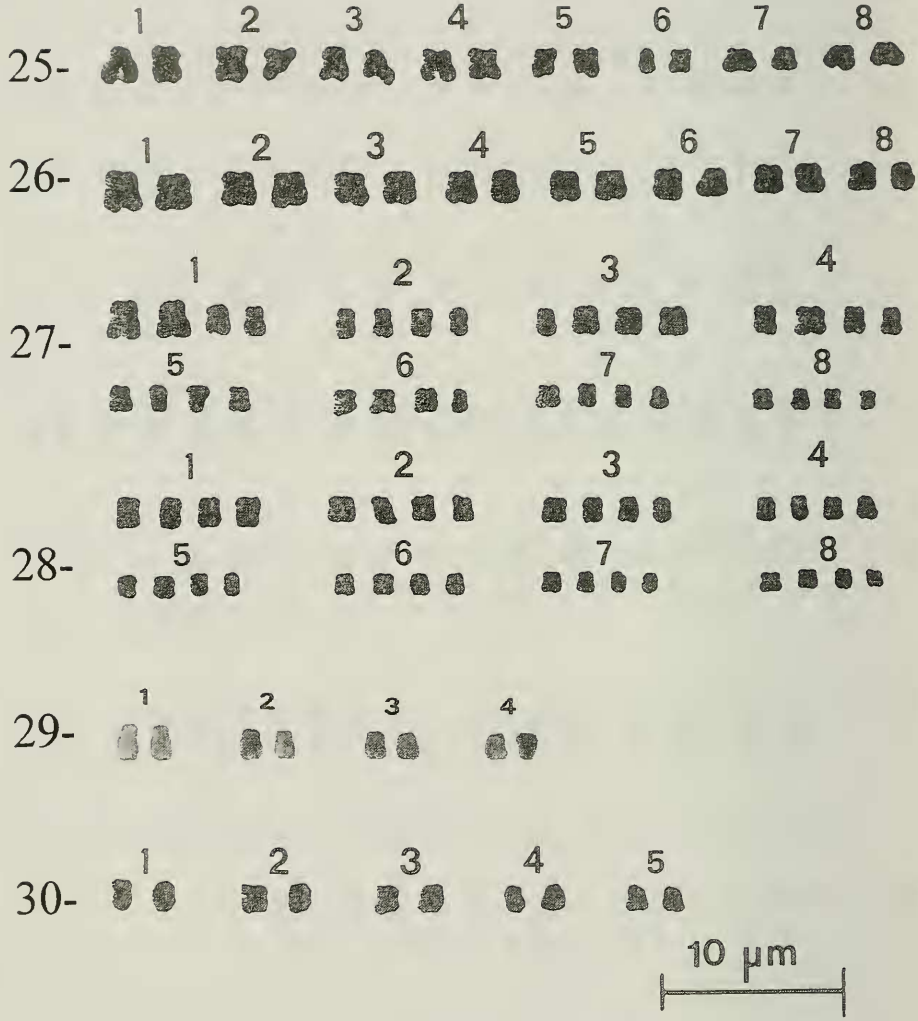

Fig 5. Karyotype of the studied taxa of tribe Cichorieae (Asteraceae)

(25) *Reichardia picroides* (26) *R. tingitana*
(27) *Sonchus macrocarpus* (28) *S. oleraceus*
(29) *Thrincia tripolitana* (30) *Urospermum picroides*

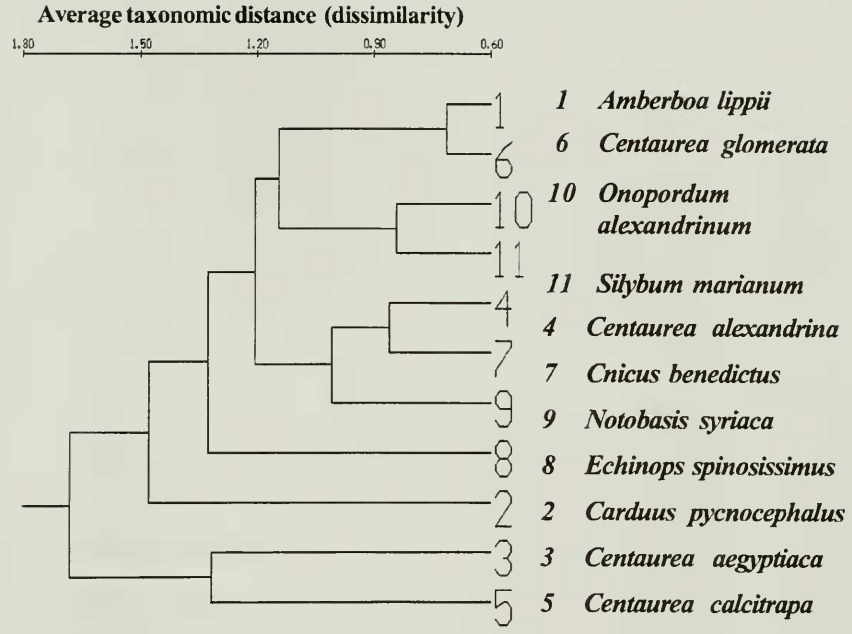

Fig. 6. UPGMA phenogram of the eleven taxa of tribe Cardueae (1-11)

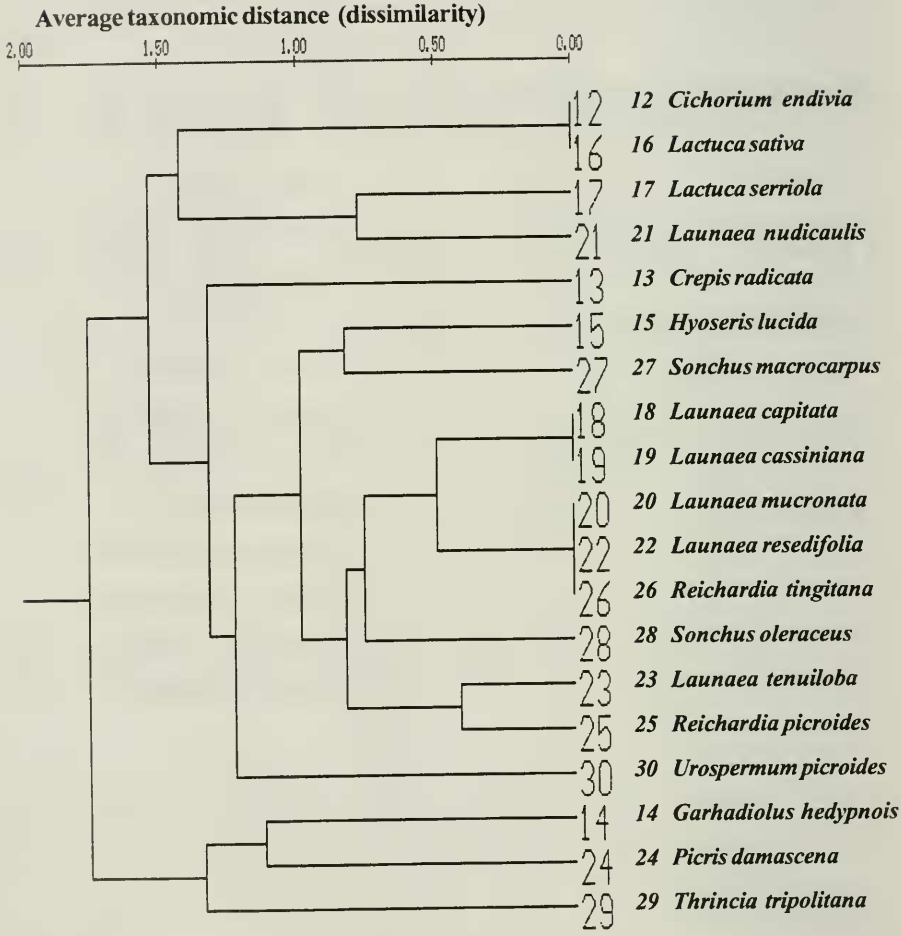

Fig. 7. UPGMA phenogram of the nineteen taxa of tribe Cichorieae (12–30)

Table 1. The cytological features of the studied taxa

No.	Tribe	Taxa	x	2n	MCL ± SE (µm)	MAR ± SE	TF %	A_1	A_2	SAT	Chr. type		
											M	m	sm
1	Carduеae	*Amberboa lippii* (L.) DC.	8	32	1.35 ± 0.09	1.20 ± 0.02	45.52	0.16	0.19	-	-	8	-
2	"	*Carduus pycnocephalus* L.	9	54	1.34 ± 0.14	1.30 ± 0.02	43.64	0.23	0.31	-	-	9	-
3	"	*Centaurea aegyptiaca* L.	8	16	2.07 ± 0.15	1.55 ± 0.21	39.93	0.29	0.21	-	-	7	1
4	"	*C. alexandrina* DEL.	10	20	1.93 ± 0.07	1.35 ± 0.06	42.67	0.25	0.12	-	-	9	1
5	"	*C. calcitrapa* L.	10	20	2.38 ± 0.21	1.56 ± 0.09	38.80	0.33	0.27	+	-	7	3
6	"	*C. glomerata* VAHL	10	40	1.95 ± 0.11	1.19 ± 0.05	45.77	0.15	0.18	-	-	10	-
7	"	*Cnicus benedictus* L.	11	22	1.44 ± 0.08	1.40 ± 0.13	42.47	0.24	0.19	-	-	10	1
8	"	*Echinops spinosissimus* TURRA	14	28	1.86 ± 0.15	1.27 ± 0.05	44.22	0.19	0.30	-	-	13	1
9	"	*Notobasis syriaca* (L.) CASS.	17	34	2.01 ± 0.06	1.35 ± 0.07	42.94	0.23	0.12	-	-	16	1
10	"	*Onopordum alexandrinum* BOISS.	17	34	1.28 ± 0.06	1.12 ± 0.03	47.14	0.10	0.20	-	2	15	-
11	"	*Silybum marianum* (L.) GAERTN.	17	34	1.14 ± 0.04	1.16 ± 0.04	46.32	0.13	0.15	-	3	14	-
12	Cichorieae	*Cichorium endivia* L.	9	18	2.03 ± 0.18	1.49 ± 0.09	39.88	0.31	0.26	-	-	6	3
13	"	*Crepis radicata* FORSSK.	8	16	2.89 ± 0.16	1.47 ± 0.08	40.41	0.31	0.16	+	-	6	2
14	"	*Garhadiolus hedypnois* (FISH. et MEY.) JAUB. et SP.	6	12	2.99 ± 0.23	2.07 ± 0.29	34.00	0.46	0.19	-	-	2	4
15	"	*Hyoseris lucida* L.	8	16	1.92 ± 0.09	1.12 ± 0.03	47.27	0.10	0.13	-	1	7	-
16	"	*Lactuca sativa* L.	9	18	2.39 ± 0.21	1.65 ± 0.17	37.69	0.35	0.26	-	-	6	3
17	"	*L. serriola* L.	9	18	2.56 ± 0.09	1.35 ± 0.06	42.62	0.25	0.10	-	-	9	-
18	"	*Launaea capitata* (SPRENG.) DANDY	8	32	1.79 ± 0.07	1.17 ± 0.03	46.15	0.14	0.11	-	-	8	-
19	"	*L. cassiniana* (JAUB. et SP.) KUNTZE	8	32	1.72 ± 0.08	1.27 ± 0.07	44.24	0.20	0.14	-	-	8	-
20	"	*L. mucronata* (FORSSK.) MUSCHLER	8	16	1.70 ± 0.10	1.21± 0.03	45.14	0.17	0.17	-	-	8	-
21	"	*L. nudicaulis* (L.) HOOK. f.	9	18	2.47 ± 0.07	1.37 ± 0.08	42.65	0.25	0.09	+	-	8	1
22	"	*L. resedifolia* (L.) KUNTZE	8	16	1.86 ± 0.09	1.25 ± 0.07	44.81	0.18	0.13	-	-	8	-
23	"	*L. tenuiloba* (BOISS.) KUNTZE	8	16	1.72 ± 0.11	1.31 ± 0.08	43.36	0.21	0.18	-	-	8	-
24	"	*Picris damascena* BOISS. et GAILL.	5	10	2.67 ± 0.24	1.84 ± 0.08	35.53	0.45	0.20	-	-	1	4
25	"	*Reichardia picroides* (L.) ROTH	8	16	1.74 ± 0.11	1.31 ± 0.07	43.58	0.22	0.18	-	-	7	1
26	"	*R. tingiana* (L.) ROTH	8	16	1.85 ± 0.07	1.20 ± 0.04	45.77	0.16	0.11	-	-	8	-
27	"	*Sonchus macrocarpus* BOULOS & JEFFREY	8	32	1.50 ± 0.08	1.11 ± 0.05	47.42	0.09	0.15	-	-	8	-
28	"	*S. oleraceus* L.	8	32	1.30 ± 0.08	1.11 ± 0.03	47.55	0.19	0.17	-	1	7	-
29	"	*Thrincia tripolitana* SCH. BIP.	4	8	1.90 ± 0.16	1.89 ± 0.29	35.00	0.42	0.16	-	-	1	3
30	"	*Urospermum picroides* (L.) DESF.	5	10	1.56 ± 0.06	1.22 ± 0.09	45.01	0.17	0.09	-	-	5	-

MCL = Mean Chromosome Length
MAR = Mean Arm Ratio
M = Metacentric chromosome
SE = Standard Error
A_1 = intrachromosomal asymmetry index
m = metacentric region chromosome
sm = submetacentric chromosome
Chr. = Chromosome
TF % = Total Form percent
A_2 = interchromosomal asymmetry ind

Table 2. The cytological characters and its codes of the studied taxa

No.	Attributes	OTU's																													
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
1	Basic Chromosome number (n=4)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
2	Basic Chromosome number (n=5)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
3	Basic Chromosome number (n=6)	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	Basic Chromosome number (n=8)	1	0	1	0	0	0	0	0	0	0	0	0	1	0	1	0	0	1	1	1	0	1	1	0	1	1	1	1	0	0
5	Basic Chromosome number (n=9)	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	1	1	0	0	0	1	0	0	0	0	0	0	0	0	0
6	Basic Chromosome number (n=10)	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7	Basic Chromosome number (n=11)	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
8	Basic Chromosome number (n=14)	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
9	Basic Chromosome number (n=17)	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10	Polyploidy Presence	1	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	1	1	0	0
11	Presence of the SAT	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
12	Chromosome Length: (1 – 2 μm)	1	1	0	1	0	1	1	1	0	1	1	0	0	0	1	0	0	1	1	1	0	1	1	0	1	1	1	1	1	1
13	Chromosome Length: (Above 2 μm)	0	0	1	0	1	0	0	0	1	0	0	1	1	1	0	1	1	0	0	0	1	0	0	1	0	0	0	0	0	0
14	Arm Ratio: 1 – 1.7	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	0	1	1	1	1	0	1
15	Arm Radio: 1.7 – 3	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0
16	Total Form Percent: TF %(30 – 40%)	0	0	1	0	1	0	0	0	0	0	0	1	0	1	0	1	0	0	0	0	0	0	0	1	0	0	0	0	1	0
17	Total Form Percent: TF %(40 – 50%)	1	1	0	1	0	1	1	1	1	1	1	0	1	0	1	0	1	1	1	1	1	1	1	0	1	1	1	1	0	1
18	Chromsome Type: M	0	0	0	0	0	0	0	0	0	1	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
19	Chromsome Type: m	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
20	Chromsome Type: sm	0	0	1	1	1	0	1	1	1	0	0	1	1	1	0	1	0	0	0	0	1	0	0	1	1	0	0	0	1	0
21	A_1 Index: 0.00 – 0.10	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
22	A_1 Index: 0.10 – 0.20	1	0	0	0	0	1	0	1	0	0	1	0	0	0	0	0	0	1	1	1	0	1	0	0	0	1	0	1	0	1
23	A_1 Index: 0.20 – 0.30	0	1	1	1	0	0	1	0	1	0	0	0	0	0	0	0	1	0	0	0	1	0	1	0	1	0	0	0	0	0
24	A_1 Index: 0.30 – 0.40	0	0	0	0	1	0	0	0	0	0	0	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
25	A_1 Index: 0.40 – 0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0
26	A_2 Index: 0.00 – 0.10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	1
27	A_2 Index: 0.10 – 0.20	1	0	0	1	0	1	1	0	1	1	1	0	1	1	1	0	0	1	1	1	0	1	1	1	1	1	1	1	1	0
28	A_2 Index: 0.20 – 0.30	0	0	1	0	1	0	0	1	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
29	A_2 Index: 0.30 – 0.40	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0